

1646

RAW SEQUENCE LISTING DATE: 11/29/2000  
PATENT APPLICATION: US/09/394,020B TIME: 16:13:44

Input Set : A:\Huv3201.app  
Output Set: N:\CRF3\11292000\I394020B.raw

3 <110> APPLICANT: PEPICELLI, CARMEN V.  
4 LEWIS, PAULA M.  
5 MCMAHON, ANDREW P.  
7 <120> TITLE OF INVENTION: REGULATION OF LUNG TISSUE BY HEDGEHOG-LIKE POLYPEPTIDES,  
8 AND FORMULATIONS AND USES RELATED THERETO  
10 <130> FILE REFERENCE: HUV-032.01  
12 <140> CURRENT APPLICATION NUMBER: 09/394,020B  
13 <141> CURRENT FILING DATE: 1999-09-10  
15 <150> PRIOR APPLICATION NUMMR: 60/099,952  
16 <151> PRIOR FILING DATE: 1998-09-11  
18 <160> NUMBER OF SEQ ID NOS: 30  
20 <170> SOFTWARE: PatentIn Ver. 2.1  
22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 1277  
24 <212> TYPE: DNA  
25 <213> ORGANISM: Gallus sp.  
27 <220> FEATURE:  
28 <221> NAME/KEY: CDS  
29 <222> LOCATION: (1)..(1275)  
31 <400> SEQUENCE: 1  
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33 Met Val Glu Met Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile  
34 1 5 10 15  
36 tgc gct ctt tta gtc tcc tct ggg ctg act tgt gga cca ggc agg ggc 96  
37 Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly  
38 20 25 30  
40 att gga aaa agg agg cac ccc aaa aag ctg acc ccg tta gcc tat aag 144  
41 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys  
42 35 40 45  
44 cag ttt att ccc aat gtg gca gag aag acc cta ggg gcc agt gga aga 192  
45 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg  
46 50 55 60  
48 tat gaa ggg aag atc aca aga aac tcc gag aga ttt aaa gaa cta acc 240  
49 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr  
50 65 70 75 80  
52 cca aat tac aac cct gac att att ttt aag gat gaa gag aac acg gga 288  
53 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly  
54 85 90 95  
56 gct gac aga ctg atg act cag cgc tgc aag gac aag ctg aat gcc ctg 336  
57 Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu  
58 100 105 110  
60 gcg atc tgc gtg atg aac cag tgg ccc ggg gtg aag ctg cgg gtg acc 384  
61 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr  
62 115 120 125  
64 gag ggc tgg gac gag gat ggc cat cac tcc gag gaa tcc ctg cac tac 432  
65 Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr  
66 130 135 140

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68 gag ggt cgc gcc gtg gac atc acc acg tcg gat cgg gac cgc agc aag 480
69 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
70 145 150 155 160
72 tac gga atg ctg gcc cgc ctc gcc gtc gag gcc gcc ttc gac tgg gtc 528
73 Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
74 165 170 175
76 tac tac gag tcc aag cgc cac atc cac tgc tcc gtc aaa gca gaa aac 576
77 Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
78 180 185 190
80 tca gtg gca gcg aaa tca gga gcc tgc ttc cct gcc tca gcc aca gtg 624
81 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
82 195 200 205
84 cac ctg gag cat gga gcc acc aag ctg gtg aag gac ctg agc cct ggg 672
85 His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
86 210 215 220
88 gac cgc gtg ctg gct gct gac gcg gac gcc cgg ctg ctc tac agt gac 720
89 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
90 225 230 235 240
92 ttc ctc acc ttc ctc gac cgg atg gac agc tcc cga aag ctc ttc tac 768
93 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
94 245 250 255
96 gtc atc gag acg cgg cag ccc cgg gcc cgg ctg cta ctg acg gcg gcc 816
97 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
98 260 265 270
100 cac ctg ctc ttt gtg gcc ccc cag cac aac cag tcg gag gcc aca ggg 864
101 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
102 275 280 285
104 tcc acc agt gcc cag gcg ctc ttc gcc agc aac gtg aag cct gcc caa 912
105 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
106 290 295 300
108 cgt gtc tat gtg ctg gcc gag gcc ggg cag cag ctg ctg ccg gcg tct 960
109 Arg Val Tyr Val Leu Gly Glu Gly Gln Gln Leu Leu Pro Ala Ser
110 305 310 315 320
112 gtc cac agc gtc tca ttg cgg gag gag gcg tcc gga gcc tac gcc cca 1008
113 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
114 325 330 335
116 ctc acc gcc cag gcc acc atc ctc atc aac cgg gtg ttg gcc tcc tgc 1056
117 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
118 340 345 350
120 tac gcc gtc atc gag gag cac agt tgg gcc cat tgg gcc ttc gca cca 1104
121 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
122 355 360 365
124 ttc cgc ttg gct cag ggg ctg ctg gcc gcc ctc tgc cca gat ggg gcc 1152
125 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
126 370 375 380
128 atc cct act gcc gcc acc acc acc act gcc atc cat tgg tac tca cgg 1200
129 Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
130 385 390 395 400
132 ctc ctc tac cgc atc gcc agc tgg gtg ctg gat ggt gac gcg ctg cat 1248

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Input Set : A:\Huv3201.app  
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133 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
134                               405 410 415
136 ccg ctg ggc atg gtg gca ccg gcc agc tg 1277
137 Pro Leu Gly Met Val Ala Pro Ala Ser
138                               420 425
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141 <211> LENGTH: 1190
142 <212> TYPE: DNA
143 <213> ORGANISM: Murine sp.
145 <220> FEATURE:
146 <221> NAME/KEY: CDS
147 <222> LOCATION: (1)..(1188)
149 <400> SEQUENCE: 2
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152 1 5 10 15
154 gca cta tct gcc cag agc tgc ggg ccg ggc cga gga ccg gtt ggc cgg 96
155 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
156 20 25 30
158 cgg cgt tat gtg cgc aag caa ctt gtg cct ctg cta tac aag cag ttt 144
159 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
160 35 40 45
162 gtg ccc agt atg ccc gag cgg acc ctg ggc gcg agt ggg cca gcg gag 192
163 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
164 50 55 60
166 ggg agg gta aca agg ggg tgc gag cgc ttc cgg gac ctc gta ccc aac 240
167 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
168 65 70 75 80
170 tac aac ccc gac ata atc ttc aag gat gag aac agc ggc gca gac 288
171 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
172 85 90 95
174 cgc ctg atg aca gag cgt tgc aaa gag cgg gtg aac gct cta gcc atc 336
175 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
176 100 105 110
178 gcg gtg atg aac atg tgg ccc gga gta cgc cta cgt gtg act gaa ggc 384
179 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
180 115 120 125
182 tgg gac gag gac ggc cac cac gca cag gat tca ctc cac tac gaa ggc 432
183 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
184 130 135 140
186 cgt gcc ttg gac atc acc acg tct gac cgt gac cgt aat aag tat ggt 480
187 Arg Ala Leu Asp Ile Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
188 145 150 155 160
190 ttg ttg gcg cgc cta gct gtg gaa gcc gga ttc gac tgg gtc tac tac 528
191 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
192 165 170 175
194 gag tcc cgc aac cac atc cac gta tgc gtc aaa gct gat aac tca ctg 576
195 Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
196 180 185 190

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Output Set: N:\CRF3\11292000\I394020B.raw

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198 gcg gtc cga gcc gga ggc tgc ttt ccg gga aat gcc acg gtg cgc ttg 624
199 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
200      195      200      205
202 cgg aqc qgc gaa cgg aag ggg ctg aqg gaa cta cat cgt qgt gac tgg 672
203 Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
204      210      215      220
206 gta ctg gcc gct gat gca gcg ggc cga gtg gta ccc acg cca gtg ctg 720
207 Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
208 225      230      235      240
210 ctc ttc ctg gac cgg gat ctg cag cgc cgc gcc tgc ttc gtg gct gtg 768
211 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
212      245      250      255
214 gag acc gag cgg cct ccg cgc aaa ctg ttg ctc aca ccc tgg cat ctg 816
215 Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
216      260      265      270
218 gtg ttc gct gct cgc gga cca gcg cct gct cca qgt gac ttt gca ccg 864
219 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
220      275      280      285
222 gtg ttc gcg cgc cgc tta cgt gct ggc gac tgc gtg ctg gct ccc ggc 912
223 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
224      290      295      300
226 ggg gac gcg ctc cag ccg gcg cgc gta gcc cgc gtg gcg cgc gag gaa 960
227 Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
228 305      310      315      320
230 gcc gtg ggc gtg ttc gca ccg ctc act gcg cac ggg acg ctg ctg gtc 1008
231 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
232      325      330      335
234 aac gac gtc ctc gcc tcc tgc tac gcg gtt cta gag agt cac cag tgg 1056
235 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
236      340      345      350
238 gcc cac cgc gcc ttc gcc cct ttg cgg ctg ctg cac gcg ctc ggg gct 1104
239 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
240      355      360      365
242 ctg ctc cct ggg ggt gca gtc cag ccg act ggc atg cat tgg tac tct 1152
243 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
244      370      375      380
246 cgc ctc ctt tac cgc ttg gcc gag gag tta atg ggc tg 1190
247 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
248 385      390      395

251 <210> SEQ ID NO: 3
252 <211> LENGTH: 1281.
253 <212> TYPE: DNA
254 <213> ORGANISM: Murine sp.
256 <220> FEATURE:
257 <221> NAME/KEY: CDS
258 <222> LOCATION: (1)..(1233)
260 <400> SEQUENCE: 3
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262 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu

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## VERIFICATION SUMMARY

DATE: 11/29/2000

PATENT APPLICATION: US/09/394,020B

TIME: 16:13:45

Input Set : A:\Huv3201.app

Output Set : N:\CRF3\11292000\I394020B.raw

L:734 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:1628 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15  
L:1628 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15  
L:1628 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15  
L:2195 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21  
L:2258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2539 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2542 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2557 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2563 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22